## EXHIBIT D 09/843,159

				,	
	ID NO:1			3045 3797	nt vs. nt
	g matrix: , gap ; identity;	penalties: - Global al	12/-2 .ignment sc	ore: -507	
		10	5	20 3	0
778106	ATGGCGG.		CTTCGGATA	AGCTCTATCG	AGTCG-AGTAC-
_	CTTTGAAGACACTGG	ATTTCATACTTT 20		PATCTCTCT-G 40	TGTCTCACTACA 50
778106	40 GCCAAGAGC	50 GG-GCGC	(	60 SCCTCTTGCA-	
	: ::: :::				
	TAGACAAATATTAGC				TCCCCCAGTTTA
(		80			110
	70		90		
778106	AGAAATGCAGC	:::: :	:::::::	: :::	: :::
- 1:	GCAGAAACATTCTGT 20 130	140			170
	110 120 -TCATGGTGCAGT		λ	140 -TGCAAAAGTC	
,,0100	:::: ::: :	::: :::	:	: ::: : ::	: : ::
- 18	ATCATAAGGTTGTGA		AGTTTTATACT	TTTGAACA-TC	
778106	TACCACTTCTCCT		AAGGTGGGCC	ACTCCATCCGG	CACCCTGA-CGT
		: :: ::			:: ::: : :
-	CATACTAAATATGCA 240 250			280	290
770106	210 TGAGGT			240	
//0106			:::: :: :	GGGAIGAICA	
-	TCAGTCACTTATTTT				
778106	260 27 AAGAAG-ACAGCGGA	0 280 AGCTG-GAGGAG			300 .GGATGGAATTGG
	: : :: : :	::: ::::	: : :	::: ::	: :: ::::
-	CTTAGGTACCACTGC 360 3	TGCTTAGTGGAG 70 380		rggctttatca 90 40	
	210 220	330	340	350	260
	310 320 TAGCAAGGCAGAGAA				360 AAGTCCAACA
_		::: : ::: GACG-TAGTTGA			:::: :::: AAGTGTCCAA
	4	20 43	0 440	0 450	460
	370	380	390	400	410
778106	GAAGTACGTGCAA	GGGGTGTAT ::::	GGAGAAGATA	GAAAAGGGCCA	
_	GCACGTGATGAT		CCTCTTCATA		
	•				
-	20	430		450	
778106	CAAGAAGA				
	::::::: GAAGTAGTCAATCTC	: :: ::: CTTTTGCGACAT			
_					

	520	530	540	550	560	570
778106	GCTGGTACC : ::	ATCCAGGCTG	CTTTGTCAAC	SAACAGGGAGG	: ::::	CCGGCCCGAGT:
_	580	590			620	
778106			GGGCTTCAG	CCTCCT	TTGCTACAGAG	580 GGATAAAGA-AG
-		GTTACAGCAT	'GGAGCTGAGC		SAAATACAGAT	GG-AAGGACAG 680
778106	CCCTGAAGA	90 \-AGCAGCTCC ::::: :::	C	GGAGTCAAGA	AGTGAAGGAA <i>I</i>	630 AGAGAAAAGGCG
-	CATTGGATT 690	TAGCAGATCC 700	ATCTGCCAAA 710		ACTGGTGAATA 730	ATAAGAAAGATG 740
778106		SATGGAGTGGA		SAAGAAGAAA-		
-			CAGGAGTGGCA		AATGATGGCT	CCTACTCACACC 800
778106	AGAAAAAGA		GTAAGCTTGA	AAAAGCCCTA	AAAGGCTCAGA	730 AACGACCTGATC
-	ATTAAATGT	::: : CAACTGCCAC	GCAAGTGA		AAAGTCAAG	: : :: CTCCATTACATT 850
778106	::: :: :	CAAGGACGAGC	TAAAGAAACT ::::	GTGTTCAACT	rAATGA	
-	860			890		ACATGGAGCTGA 910
778106	TACTCATCT	: :: : :	GCAA(	STGCCTTCTGC :::::::: STACCAT-TAC	: : : CACAATGCCT	GATCTTGGAC :::::::::::::::::::::::::::::::::::
778106		850	860	870	880	
_	::	:: : :: STAACTGAACT	:::: TTTGGTCAAC	:::::: GCATGGTGCC-	: : ::	::::::: GCAATGGACT
778106		CTGGTCT	TCAAGAGCG		CTGCACTGGG	950 GACGTCACTGC-
- 1				CAGCTTCTAAC 1060		SAAGTATGTTCT 1080
	:: : :	AGTGTATGGT(	:::: :: :	ACACCCAA	ACCGG	AAG ::: PAAAAGTGCTAT
<del>-</del> .		1100				
778106	-GAGTGGGT		GAATTCCGA	SAAATCTCTTA	ACCTCAAGAA	1050 ATTGAAGGTTAA :::::::

	AGACTTGGCTC	CCACACCAC	CAGTTAAAA	GAAAGATTAG	CATATGAATTT	TAAAGGCCAC
_	1150 1	.160	1170	1180	1190	1200
779106	77	1060		1070 ATATTCCCCC		1090
778100				:: :: : :		
-				ATGTTACTCGAA 1240		TCTCTCTCTG 1260
778106	TGGCGGC	CCACGCC	CTCCGCCCT	1120 CCACAG : ::::	CCTCGGCTCCT	GCTGCTGTG
_	GAAATGGTGAA	ATTTCAAGC	TCCTCAAA	CACATGAAACAG 1300	CATTGCATTGT	rgctgctgc-
770106				170 118		
110100				::: ::		
_				ATATGTG 50		
121	00 1210	) 122	20 13	230 1	240 13	250
	GCTGTCCCGG	ACAAGGATO	SAAGTGAAG	GCCATGATTO	SAGAAACTCGG(	GGGAAGTTG
_		AGCAAACATO	CAATGAAAA	GACTAAAGAATT 1400	CTTGACTCCT	CTGCACGTGG
	1260				1290	
778106			GCTTCCCT- : : :	GT ::	GCATCA-GCAC	
_	CATCTGAGAAA	AGCTCATAA	GATGTTGT	rgaagtagtggi 1460	GAAACATGAA	
		1320				1340
778106	AGGAGGTGGA	AAGATGAA	TAAGA		AGATGGA	GGAAGTAAAG
778106	AGGAGGTGGAZ : : :::: ATGCTCTGGAT	AAAGATGAAT :: : : CAATCTTGGT	PAAGA : ::: PCAGACTTC	rctacacagago	AGATGGAC : :: : CTGCATATTGTC	GGAAGTAAAG :: : : GGTCATCTAC
778106	AGGAGGTGGAZ : : :::: ATGCTCTGGAT	AAAGATGAAT :: : : CAATCTTGGT	PAAGA : ::: PCAGACTTC		AGATGGAC : :: : CTGCATATTGTC	GGAAGTAAAG :: : : GGTCATCTAC
_	AGGAGGTGGAZ : : :::: ATGCTCTGGAT 1490	AAAGATGAAT :: : : CAATCTTGGT 1500	TAAGA : ::: TCAGACTTC 1510	ICTACACAGAGO 1520 1370	AGATGGAG : :: : CTGCATATTGTG 1530	GGAAGTAAAG :: : : GGTCATCTAC 1540 1380
_	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: :::	AAAGATGAAT :::::::::::::::::::::::::::::	TAAGA : ::: TCAGACTTC 1510  1360 GAGTTGTGTGT	TCTACACAGAGC 1520 1370 CTGAGGACTT	AGATGA( ::::: CTGCATATTGT( 1530	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: :::: :
_	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: :: AAACCTGCCGG	AAAGATGAAT :::::::::::::::::::::::::::::	TAAGA TAAGA TCAGACTTC 1510  1360 GAGTTGTGTGT TTTTTTTTTTTTTTTTTTTTTTTTTT	FCTACACAGAGO 1520 1370 CTGAGGACTT	AGATGA( ::::: CTGCATATTGT( 1530 C( : ACATTATATCC(	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : : CTTCAGGGCT
- 778106 -	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: :: AAACCTGCCGG 1550  1390 TCTCCGCCTCG	AAAGATGAAT :::::::::::::::::::::::::::::	TAAGA TAAGACTTC TCAGACTTC 1510  1360 SAGTTGTGTGT TO TATE TAGGACTATGGG TS70  CCTT	TCTACACAGAGG 1520 1370 CTGAGGACTT :: : : STGTGATCCTAA 1580 1410CAGGAGTT	AGATGAG : :::: CTGCATATTGTG 1530CG :: ACATTATATCCG 1590 1420 CGTTCTTAGCGG	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : CTTCAGGGCT 1600  1430 CACATCTTGT
- 778106 -	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: ::: AAACCTGCCGG 1550  1390 TCTCCGCCTCG: :::: TTACTGCTTTM	AAGATGAAT  :::::::::::::::::::::::::::::	TAAGA : ::: TCAGACTTC' 1510  1360 GAGTTGTGTG' ::: ::: GAGCTATGGG 1570  CCTT : AAATGAAAA	TCTACACAGAGC 1520 1370 CTGAGGACTT :: : : GTGTGATCCTAA 1580 1410	TACATTATATCC  1420  CETTCCTAGGGGGC  CCTCCAAGAGGGGGCC  CCTCCAAGAGGGCC  CCTCCCAAGAGGGCC  CCTCCCAAGAGGCC  CCTCCCAAGAGCC  CCTCCCAACAGGCC  CCTCCCAACAGCC  CCTCCCAACAGCC  CCTCCCAACAGCC  CCTCCCAACACC  CCTCCCACACC  CCTCCCAACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCACACC  CCTCCCCCCCC	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : GGTATCTCAT
- 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: :: AAACCTGCCGG 1550  1390 TCTCCGCCTCG: : ::: TTACTGCTTTM 1610  1440	AAAGATGAAT :::::::::::::::::::::::::::::	TAAGA TAAGA TAAGACTTC' 1510  1360 GAGTTGTGTG' TAAGACTATGGG' 1570  CCTT TAAATGAAAA' 1630	TCTACACAGAGG 1520  1370 CTGAGGACTT ::::::::::::::::::::::::::::::::::	TGCATATATCC  1530  CACATTATATCCC 1590  1420 CACTTCTTAGCGC :: :: :: :: :: :: :: :: :: :: :: :: ::	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : : GGTATCTCAT 1660  1480
- 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: ::: AAACCTGCCGG 1550  1390 TCTCCGCCTCG: :::: TTACTGCTTTM 1610  1440 CCCCTTGG	AAAGATGAAT :::::::::::::::::::::::::::::	TAAGA : ::: TCAGACTTC' 1510  1360 GAGTTGTGTG' ::: ::: GAGCTATGGG 1570  CCTT : AAATGAAAA' 1630	TCTACACAGAGG 1520  1370 CTGAGGACTT :: : : STGTGATCCTAA 1580  1410CAGGAGTT ::: : : FGTACAGCAACT 1640	TACATTATATCC  1530  ACATTATATCC  1590  1420  CGTTCTTAGCGG  1650  1470  CAGAGGCCTGTTC	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : GGTATCTCAT 1660  1480 GAAGTTGTGG GAAGTTGTGG
- 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: ::: AAACCTGCCGG 1550  1390 TCTCCGCCTCG: :::: TTACTGCTTTM 1610  1440 CCCCTTGG : : : TAGGTAATTCM	AAGATGAAT  :::::::: AATCTTGGT  1500  1350 CCAACATCCC  ::::::::: CCTACTCCTC  1560  1400 CACCAAGAGG  ::::::: ACAGATGGGA  1620  1450 GGGGGCAGA- :::::::: AGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	TAAGA TAAGA TAAGACTTC' 1510  1360 GAGTTGTGTG' TAAGACTATGG' 1570  CCTT TAAATGAAAA' 1630  CAGACAATTC	1370 1370 CTGAGGACTT ::::::: STGTGATCCTAA 1580 1410CAGGAGTT :::::::: IGTACAGCAACT 1640 1460 GGTG-AAGGG	TAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : GGTATCTCAT 1660  1480 GAAGTTGTGG :: : : : GAAGTTGTGG
- 778106 - 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGG :: ::: AAACCTGCCGG 1550  1390 TCTCCGCCTCG: :::: TTACTGCTTTM 1610  1440 CCCCTTGG : : TAGGTAATTCM 1670  CCCCCAAGA	AAGATGAAT  :::::::: AATCTTGGT  1500  1350 CCAACATCCC  :::::::: CCTACTCCTC  1560  1400 CACCAAGAGG  :::::: ACAGATGGGA  1620  1450 GGGGGCAGA- :::::::: AGAGGCAGAC  1680  1490GGGAAG	TAAGA TAAGA TAAGA TCAGACTTC' 1510  1360 GAGTTGTGTG' TSAGCTATGGG 1570  CCTT TAAATGAAAA' 1630  CAGACAATTG 1690  1500 TCAGGGG	1370 1370 2TGAGGACTT ::::::::::::::::::::::::::::::::::	TAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : GGTATCTCAT 1660  1480 GAAGTTGTGG :: : : : GATGTCGAAA 1720  AAGGGC
- 778106 - 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGC :: ::: AAACCTGCCGC 1550  1390 TCTCCGCCTCC : :::: TTACTGCTTTM 1610  1440 CCCCTTGC : : TAGGTAATTCM 1670  CCCCAAGA : ::: CTGTAAAAAAM	AAGATGAAT  :::::::: AATCTTGGT  1500  1350 CCAACATCCC  :::::::: CCTACTCCTC  1560  1400 CACCAAGAGGC  ::::::: ACAGATGGGA  1620  1450 GGGGGCAGA- :::::::: AGAGGCAGAG  1680  1490GGGAAG  ::::::: ACTGTGTAC	TAAGA TAAGA TAAGA TCAGACTTC' 1510  1360 GAGTTGTGTG' TSAGCTATGG' 1570  CCTT TAAATGAAAA' 1630  CAGACAATTC 1690  1500 TCAGGG' TCAGGG' TGTTCAGAG	1370 1370 CTGAGGACTT ::::::::::::::::::::::::::::::::::	TAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : : GGTATCTCAT 1660  1480 GAAGTTGTGG :: : : : GATGTCGAAA 1720  AAGGGC ::::: AAGGGCGTCA
- 778106 - 778106 - 778106 - 778106	AGGAGGTGGAM : : :::: ATGCTCTGGAM 1490  GAAGC :: ::: AAACCTGCCGC 1550  1390 TCTCCGCCTCC : : ::: TTACTGCTTTM 1610  1440 CCCCTTGC : : TAGGTAATTCM 1670  CCCCAAGA : ::: CTGTAAAAAAM 1730	AAGATGAAT  :::::::: AATCTTGGT  1500  1350 CCAACATCCCT  1560  1400 CACCAAGAGG  ::::::: ACAGATGGGA  1620  1450 GGGGGCAGA- :::::::: AGAGGCAGAG  1680  1490GGGAAGT  1740	TAAGA TAAGA TAAGA TCAGACTTC' 1510  1360 GAGTTGTGTG' TSAGCTATGGG 1570  CCTT TAAATGAAAA' 1630  CAGACAATTG 1690  1500 TCAGGGG TCAGGGG T750  1540	1370 1370 CTGAGGACTT ::::::::::::::::::::::::::::::::::	TAGATGAC  : :: ::  TGCATATTGTC  1530 CC  :  ACATTATATCCC  1590  1420  CGTTCTTAGCGC  :: :: ::  CCCTCCAAGAGC  1650  1470  CAGAGCCTGTTC  :: :: ::  CAAAGGCTGGAC  1710  1520  CAAAAAAAAGC  :: : ::  CAGAGACATTGAC  1770  1560	GGAAGTAAAG :: : : : GGTCATCTAC 1540  1380 CTCCAGGACG :: ::: : CTTCAGGGCT 1600  1430 CACATCTTGT ::: : GGTATCTCAT 1660  1480 GAAGTTGTGG :: :: : GATGTCGAAA 1720  AAGGGC ::::: AAGGGCGTCA 1780

-		CACTTCATI	TTGCAGCTGG	:::: :::: : GTAT-AACAGA( 0 1820	G-TGTCCGTGG	
778106	CTCTTAAAC	GA-GGAGC	CAGCTGTGGAT	1610 CCTGATTC	rggactgg	AACACTCTGC-
_	CTGCTACAC	GCATGGAGC	CTGATGTGCAT	GCTAAAGATAA 1870	AGGAGGCCTTG	TAC-CTTTGCA
778106	GCAT		GAGAA	1650 AGGTGG-GAAGG		1660 CAGT ::::
-		STTCTTATO	GACATTATGA	AGTTGCAGAAC 1930	TTCTTGTTAAA	CATGGAGCAGT
778106	-GCCACCCT	rtggcci	GGTGGACAT-	1690 CGTTAA	AGGAACCAACT	
_		ragctgati	TATGGAAATT	: ::: TACACCTTTACA 1990	ATGAAGCAGCA	GCAAAAGGAAA
778106		TACAAGO	CTGCAGCTTC-	1730 TGGAGGA-	CGAC-AAG	GAAAACAGGTA
	ATATGAAA1 2020	TTTGCAAAC	CTTCTGCTCCA	::: :: GCATGGTGCAGA 2050	ACCCTACCAAA	AAAAACAGGGA
		TTCAC	GTCCTGGGGC	1780 CG-TGTGGGTA	CGGT	GATCGGTAG
-	TGGAAATA	CTCCTTTGG	SATCTTGTTAA	: :: : :: AGATGGAGATA 2110		GATCTGCTTAG
	2000	2030	2100	2110		
778106	18 CAAC	300 AAACTGGAA	1810 ACAGATGCCGT	1820 CCAAGGAGGAT	1830 GCCAT	TGAGCA
778106 -	18 CAACA : GGGAGATGG	300 AAACTGGAA : :: CAGCTTTGC	1810 ACAGATGCCGT :::::::	1820	1830 GCCAT :::: TGTTTAGCCAG	TGAGCA : : : AGTGAAGAAGT
- *	1840 CTTC	300 AAACTGGAA : :: CAGCTTTGC 2150	1810 ACAGATGCCGT ::::::: CTAGATGCTG- 2160 1850 TG-AAATT	1820 CCAAGGAGGAT ::::: :::: CCAAGAAGGGT 2170	1830 GCCAT :::: TGTTTAGCCAG 2180 - 1860 -GAAGAAA	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC
- *	1840 CTTC ::::	300 AAACTGGAA : :: CAGCTTTGC 2150AT	1810 ACAGATGCCGT ::::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::::	1820 CCAAGGAGGAT ::::: :::: CCAAGAAGGGT 2170	1830GCCAT :::: FGTTTAGCCAG 2180	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC
- 778106 -	1840 CTTC :::: TGTCTTCTC 2200 1880 GCTTGGCAC	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAAATTCA	1820 CCAAGGAGGAT ::::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230  1900 CGAAGTATCCC	1830GCCAT :::: TGTTTAGCCAG 2180 - 1860 -GAAGAAA ::::: GGCAGACATTC 2240  1910 AAAAAAGTTCTA	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC 2250  1920 CCCCCTGGAGA
- 778106 -	1840 CTTC::: TGTCTTCTC 2200 1880 GCTTGGCAC:::::	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210 CTCC : GCTGGTTAT	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAATTTCA ::::::	1820 CCAAGGAGGAT ::::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230	1830GCCAT :::: FGTTTAGCCAG 2180  1860 -GAAGAAA :::::: GGCAGACATTC 2240  1910 AAAAAAGTTCTA ::::: AGTATTTGTTA	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC 2250  1920 CCCCCTGGAGA : : ::: CAACACCGGAGC
- 778106 - 778106	1840CTTC :::: TGTCTTCTC 2200 1880 GCTTGGCAC ::::: ATTTAGCAC 2260 1930 TTGACTA	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210 CTCC : GCTGGTTAT 2270 1940 ATGGCCAGG	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAAATTCA :::::: TAATAATTTA- 2280  GATGAAG	1820 CCAAGGAGGAT ::::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230  1900 CGAAGTATCCC :::::::::::::::::::::::::::::::::	1830GCCAT :::: TGTTTAGCCAG 2180AGGCA 1860GAAGAAA :::::: GGCAGACATTC 2240 1910 AAAAAAGTTCTA :::::: AGTATTTGTTA 2300	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC 2250  1920 CCCCCTGGAGA : : :::: CAACACGGAGC 2310  G
- 778106 - 778106	18 CAACA : GGGAGATGG 2140 1840 CTTC :::: TGTCTTCTG 2200 1880 GCTTGGCAG ::::: ATTTAGCAG 2260 1930 TTGACTA: ::: TGATGTGAA	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210 CTCC : GCTGGTTAT 2270 1940 ATGGCCAAC	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAATTTCA :::::: TAATAATTTA- 2280  SATGAAG ::::: GACAAAGGAGG	1820 CCAAGGAGGAT :::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230  1900 CGAAGTATCCCA :::::: -GAAGTTGCAG 2290	1830GCCAT :::: TGTTTAGCCAG 2180	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC 2250  1920 CCCCCTGGAGA : : ::: CAACACGGAGC 2310  G : GCATCTTACGG
- 778106 - 778106 -	18CAACA : GGGAGATGG 2140  1840CTTC :::: TGTCTTCTC 2200  1880 GCTTGGCAG ::::: ATTTAGCAG 2260  1930 TTGACTA: ::: TGATGTGAA 2320	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210 CTCC : GCTGGTTAT 2270 ATGGCCAAC 2330 1960 -TGAAGAAC	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAATTTCA :::::: TAATAATTTA- 2280  GATGAAG ::::: GACAAAGGAGG	1820 CCAAGGAGGAT ::::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230  1900 CGAAGTATCCCA :::::: -GAAGTTGCAG 2290  ACTTATTCCTT 2350  1970 ACAGTA-AATC	1830GCCAT :::: TGTTTAGCCAG 2180	TGAGCA : : : AGTGAAGAAGT 2190  1870 AAACCGGGAAC :: : :: AACACCTTTAC 2250  1920 CCCCCTGGAGA : : ::: CAACACGGAGC 2310  G : GCATCTTACGG 2370  1990 -CCAAGTCCAA
- 778106 - 778106 -	180 CAACA : GGGAGATGG 2140  1840CTTC :::: TGTCTTCTC 2200  1880 GCTTGGCAG ::::: ATTTAGCAG 2260  1930 TTGACTA: ::: TGATGTGAA 2320  GCATGTAGA	300 AAACTGGAA : :: CAGCTTTGC 2150AT :: CCTGATAAT 2210TCC : GCTGGTTAT 2270 ATGGCCAAC 2330 1960 -TGAAGAAC :: :: ::	1810 ACAGATGCCGT :::::: CTAGATGCTG- 2160  1850 TG-AAATT :::::: TGTAAATTGCC 2220  1890 CAAAAATTTCA :::::: TAATAATTTA- 2280  SATGAAG ::::: GACAAAGGAGG 0 2340  GCTG GCTG	1820 CCAAGGAGGAT :::::::::: CCAAGAAGGGT 2170 ATAT ::: CGCGATACCCAAG 2230  1900 CGAAGTATCCCA :::::: -GAAGTTGCAG 2290  ACAGTA-AATC ::::::: CAAAGTATAATG	1830GCCAT :::: TGTTTAGCCAG 2180	TGAGCA :::: AGTGAAGAAGT 2190  1870 AAACCGGGAAC :::::: AACACCTTTAC 2250  1920 CCCCCTGGAGA :::::: CAACACGGAGC 2310  G : GCATCTTACGG 2370  1990 -CCAAGTCCAA ::::::: GCCACGGACAA

							CTTTGA
_		TTC-ACACC	CTTTGCACG	AAGCAGCC	CAAAAGGG	: ACGAACACAG 2480	CTTTGTGCTT
778106		AGTATG <i>P</i> ::::::			-AAAGCCA1	2060 rggtggagta : ::: :	TGAG
-		AGCCCATGO		CGACTCTT.	AAAAATCAG	GGAAGGACAA	: :: ACACCTTTAG 2550
778106	ATCGACC'		ATG	CCCTT	GGGGAAGCT	2110 FGAGCAAAAG :::::	GCAGATC
-	ATTTAGT	TTCAGCGG	TGATGTCA	GCGCTCTT	CTGACAGC-		CCCCATCTGC
	-CAGGCC		CA	TCCTCA	GTGAGGTC		TGTCTCAGGG
_	TCTGCCC	TCTTGTTAC	CAAGCCTCA	AGTGCTCA	ATGGTGTG-		: :: : AGGAGCCACTG 50
	CAGCAGC	GA-CTCT-C	CAGATCC-T	GGATCTCT	CAAATCGCT	2210 FTTTACACCC	TG-ATCCCCC
- 26	CAGATGC	TCTCTCTTC	CAGGTCCAT	CTAGCCCA	TCAAGCCTT		AGCAGTCTTG
778106	ACGACTT	TGGGA-		AAGCCT			2260 GAACAA
- 273	ACAACTT	ATCTGGGA	STTTTTCAG	AACTGTCT	TCAGTAGT	TAGTTCAAGT	GGAACAGAGG
	ACAACTTA 30 : 2: -TGCAGA	ATCTGGGAC 2740 270 CAGTGTGCA	ETTTTTCAG. 2750 2280 AGGCCAAGG	AACTGTCT 2760 CGGA	TCAGTAGT1 2770	ragttcaagt ) 278	2290 AATGC-
778106	ACAACTTZ 30 2: -TGCAGAG ::: GTGCTTCG	ATCTGGGAC 2740 270 CAGTGTGC <i>I</i> ::::::::: CAGTTTGG <i>I</i>	ETTTTTCAG. 2750  2280 AGGCCAAGGGGGGGGGAAAAAGGAAAAAAGG	AACTGTCT 2760  CGGA :: AGGTTCCA	TCAGTAGTI 2770	ragttcaagt ) 278 	2290 AATGC- ::::
778106	ACAACTTZ 30 2: -TGCAGAC ::: GTGCTTCC 90 :	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800	2750 2280 AGGCCAAGGGGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAA	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 IGCTGGAC	TCAGTAGTI 2770 GGAGTAGAI 2830 23 ATCGAGGT	TAGTTCAAGT ) 278 TTTTAGCATA ) 284 320 2 G-GCCTACAG	2290AATGC- :::: ACTCAATTCG 0 2330 ETCTGCTCAGG
778106	ACAACTTZ 30 2: -TGCAGAG ::: GTGCTTCG 90 2: TAAGGAA	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800	2750 2280 AGGCCAAGGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 TGCTGGAC: :::: TAATGGAT	TCAGTAGTT 2770 GGAGTAGAT 2830 23 ATCGAGGTC	TAGTTCAAGT  278  TTTTAGCATA  284  320  G-GCCTACAG  : :::: GAGAGAACAG	2290AATGC- :::: ACTCAATTCG 0 2330TCTGCTCAGG ::::: CATCACTTTGG
778106 - 279 778106 - 289	ACAACTTZ 30 2: -TGCAGAC ::: GTGCTTCC 90 2: TAAGGAA' 50 2340 GGAGGGTC	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800  TCTTGGACT 2860  2350 CTGATGATA	2750  2280 AGGCCAAGGE E :::: AGAAAAAGGE 2810  2300 ATGACAACCE E ::::::: ATGAGCACCE 2870  24GCAG	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 TGCTGGAC: :::: TAATGGAT 2880  360 CAAGGATC	TCAGTAGTT 2770 GGAGTAGAT 2830 ATCGAGGTC :: : : ATATTTGAC 2890 2370 CCATCGA	TAGTTCAAGT ) 278 TTTTAGCATA ) 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG ) 290TGTCA	2290AATGC- :::: ACTCAATTCG 0 2330 CTCTGCTCAGG :::: CATCACTTTGG 00 2380 ACCTATG-
778106 - 279 778106 - 289 778106	ACAACTTZ 30 2: -TGCAGAC ::: GTGCTTCC 90 2: TAAGGAA' 50 2340 GGAGGGTC :::	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800	2750  2280 AGGCCAAGGEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 TGCTGGAC: :::: TAATGGAT 2880  360 CAAGGATC :::::: CAAGGAGC	TCAGTAGTT 2770 GGAGTAGAT 2830 ATCGAGGTC :: :: ATATTTGAC 2890  2370 CCATCGA : :: TGAAGGAGA	TAGTTCAAGT ) 278 TTTTAGCATA ) 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG ) 290TGTCA	2290AATGC- :::: ACTCAATTCG 0 2330 CTCTGCTCAGG ::::: CATCACTTTGG 00 2380 ACCTATG- :::: AATGCTTATGG
778106 - 279 778106 - 289 778106 - 299	ACAACTTZ 30  2: -TGCAGAC ::: GTGCTTCC 90  TAAGGAAC 50  2340 GGAGGGTC :: AT-GTATC 10  23AGAAG	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800  TCTTGGACT 2860  2350 CTGATGATA ::::: TAGTTGAGA 2920  90 2 CTCAAAACT	2750  2280 AGGCCAAGG  :::::: AGAAAAAGG  2810  2300 CTGACAACC  2870  2400 CGGCATTAA	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 TGCTGGAC : :::: TAATGGAT 2880  360 CAAGGATC :::::: CAAGGAGC 294  2410 GGTGGTTG	TCAGTAGTT 2770 GGAGTAGAT 2830 ATCGAGGTC :::: ATATTTGAC 2890 CCATCGA ::: TGAAGGAGA 0 29 2420 ACAGAGAT	TAGTTCAAGT ) 278 TTTTAGCATA ) 284 320 2 G-GCCTACAG : : :::: GAGAGAACAG ) 290TGTCA :: ::: ATTGGAATCA 950 2 430 -TCTGAAGAA	2290AATGC- :::: ACTCAATTCG 0 2330 CTCTGCTCAGG ::::: CATCACTTTGG 0 2380 ACCTATG- :::: AATGCTTATGG 2960 0 2440 AGCCGAGATCA
778106 - 279 778106 - 289 778106 - 299	ACAACTTZ 30  2: -TGCAGAC ::: GTGCTTCC 90  TAAGGAA' 50  2340 GGAGGGTC :: AT-GTAT' 10  23AGAAGC :::	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800	2750  2280 AGGCCAAGG : :::: AGAAAAAGG 2810  2300 TTGACAACC 2870  2470  2400 TGACATTAA : : :::: TAATTAA	AACTGTCT 2760  CGGA :: AGGTTCCA 2820  2310 TGCTGGAC: :::: TAATGGAT 2880  360 CAAGGATC :::::: CAAGGAGC 294  2410 GGTGGTTG ::::: AGGAGTCG	TCAGTAGTT 2770 GGAGTAGAT 2830 ATCGAGGTC :::::::::::::::::::::::::::::::::::	TAGTTCAAGT ) 278	2290AATGC- :::: ACTCAATTCG 0 2330 CTCTGCTCAGG ::::: CATCACTTTGG 00 2380 AACTATG- :::: AATGCTTATGG
778106 - 279 778106 - 289 778106 - 299 778106 - 299	ACAACTTZ 30  2: -TGCAGAC ::: GTGCTTCC 90  TAAGGAA' 50  2340 GGAGGGTC :: AT-GTAT' 10  23'AGAAGC ::: ACATAGGC 2970  TCAGGAAC	ATCTGGGAC 2740  270 CAGTGTGCA :::::::: CAGTTTGGA 2800	2750  2280 AGGCCAAGG : :::: AGAAAAAGG 2810  2300 CTGACAACC 2870  2400 CTGACATTAA : : ::: TAATTAA 29 2460	AACTGTCT 2760  CGGA :: AGGTTCCA 2820 2310 TGCTGGAC: :::: TAATGGAT 2880  360 CAAGGATC :::::: CAAGGAGC 294 2410 GGTGGTTG ::::: AGGAGTCG 90  AC	TCAGTAGTT 2770  GGAGTAGAT 2830  ATCGAGGTC :::::::::::::::::::::::::::::::::::	TAGTTCAAGT ) 278	2290AATGC- :::: ACTCAATTCG 0 2330TCTGCTCAGG :::: AACTCACTTTGG 00 2380 ACTATG- :::: AATGCTTATGG 2960 0 2440 AGCCGAGATCA ::::: CAACAAGGTCT 3020

778106ACAATGCGTATGACTTGGAAGT-CA-TCGATATCT : :: :: :: :: :::: :::: ::::::::::::	0
ር ርመር እመር እመል እእር እርጥሞሞር እርጥር ምርጥር እርር እእር እእር እጥር ርእ እርሞ እርሞ እርሞ ውር እር እርር እር	
3090 3100 3110 3120 3130 3140	С
2520 2530 2540 2550 778106 TAAGATAGAGCGTGAAGGCGAATGCCAGCGTTACAAGCC-CTTTAAGCAG	G
::::::::::::::::::::::::::::::::::::::	:
2560 2570 2580 2590 778106 CTTCATAACCGAAGATTGCTGTGGCACGGGTCCAGGA	_
:: :::: ::: :: :: : : :: ::: ::: GTTTGTAACAAGAAA-CTATGGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGA	7\
3210 3220 3230 3240 3250	rs.
2600 2610 2620 2630 778106CCACCAACTTTGCTGGGATCCTGTCCCA-GGGTCTTCGGA :::::::::::::::::::::::::::::	_
- GAAAACCAC-AACCATGCCAATGAACGAATGCTATTTCATGGGTCTCCTTTTGTGAATG 3260 3270 3280 3290 3300 3310	С
2640 2650 2660 2670 2680 778106TAGCCCCGCCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAG	
AATTATCCACAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTGGAGCTG	
3320 3330 3340 3350 3360 3370	
2690 2700 2710 2720 2730 2740 778106 GATCTATTTCGCTGACATGGTCTCCAAGAGTGCCAACTACTGCCATACGTCTCAGGGAG. :: ::::: :::: ::::: ::::: :: :: :: :: :	Α
- CATTTATTTTGCTGAAAACTCTTCCAAAAGCAATCAATATGTATATGGAATTGGAGG. 3380 3390 3400 3410 3420 3430	A
2750 2760 2770 2780 2790 778106 CCCAATAGGCTTAATCCTGTTGGGAGAAGTTGCCCTTGGAAACATGTAT	G
::::::::::::::::::::::::::::::::::::::	
2800 2810 2820 2830 2840	_
778106 AACTGAAGCACGCTTCACATATCAGCAAGTTACCCAAGGGCAAGCACAGTG	
_ CTCTTTTGC-CGGGTAACCT-TGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATG 3500 3510 3520 3530 3540 3550	
2850 2860 2870 2880 778106 CAAAGGTTTGGGCAAAACTACCCCTGATCCTTCAGCTAA	
::::::::::::::::::::::::::::::::::::::	
2890 2900 2910 2920 2930 2940 778106 ATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACCGGGATTTCATCTGGTGTGAATGA	
2950 2960 2970 2980 2990 778106 ACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGGTAA	A
:: :::::::::::::::::::::::::::::::::::	.G

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3010
                    3020
778106 TCTGAAGTA--TCTGCTGAAACTGAAAT--TCAA-----TTTTAAG
      :: :: :: ::::: :::: ::::
    A---AACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGGCCTCTACGTTTTACT
         3730 3740 3750 3760 3770
        3040
778106 ACCTCCCTGTGGTAA----
    ::::::::::
    CCTTTGCTGAAAAAAAAAAA
   3780 3790
> PARP-1
                                3045 nt vs.
> SEQ ID NO:2
                               3816 nt
scoring matrix: , gap penalties: -12/-2
46.3% identity; Global alignment score: -435
                   20 30
         10
                               40
CGCGCTGCTCCGCCGCGCGGGGCAGCCGGGGGGGCAGGGAGCCCAGCGAGGGGCGCGCG
         10 20 30 40 50
                          70
    50
        60
TGGGCGCGCCCATGGGACTGCGCCGGATCCGGTGACAGCAGGGAGCCAAGCGGCCCGGG
         70 80 90
                         110 120
      90
             100
649550 -CAAGGACTCG----CTCCGGATGGCCA-----TCATGGTGCAGTCGCCCATGT
    CCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCCTGCTCGCGGGGCCGGGGCTCCTGC
           140 150 160 170
           140
                 150
                               160
649550 T----TGATGGAAAAGTCCCACACTG-----GTACCACTTCTCCT-GCTTCT
    {\tt TCCGGTTGCTGGCGTTTGCTGGCTGTGGCGGCGGCCAGGATCATGTCGGGTCGCCGCT}
        190
              200 210 220 230
        180
              190
                       200
                             210
649550 G-GAAGGTGGGCCA-CTCCATCCG---GCACC-CTGACGTTGAGGTGGATGGGTTCTCT-
    GCGCCGGCGGGGAGCGCCTGCGCGAGCGCCGAGGCCGTGGAGCCGGCCCCC
        250
           260 270 280 290 300
      230
            240
                         250
                                260
649550 --GAGCT-TCGGTGGGATGATCAGCA-----GAA--AGTCAAGAAGACAGCGGA
     GAGAGCTGTTCGAGGCGTG--CCGCAACGGGGACGTGGAACGAGTCAAGAGG-CTGGTGA
            320 330 340
        310
         280
                 290
649550 AGCTGGAGGAG-TGA-CAG--GCAAA-----GGCCAGGA------TGGAATTGG
    CGCCTGAGAAGGTGAACAGCCGCGACACGGCGGGCAGGAAATCCACCCCGCTGCACTTCG
              380 390
             320
                    330
   310
                           340
                                 350
649550 TAGCAAG-----GCAGAGAAGACTCTGGGTGACT--TTGCAGCAGAGTA-TGCCAA-GT
```

	CCGCAGGT 420	TTTGGGCGG 430	A-AAGACG-1 440	'AGTTGAATAT' 450	TTGCTTCAGAA1 460	rggtgcaaatgt 470
649550	CCAACAGA		AAGGGG	-TGTATGGAG		410 GGGCCAGGTGCĠ
_	CCAA	-GCACGTGA	TGATGGGGG			GCTCTTTTGGT 20 530
649550			TGGT	G-GACCCGGAG	450 AAGCCACAC	GCTAGGCATGAT
-	CATGCTGA	AGTAGTCAA	TCTCCTTTTC	CGACATGGTG	CAGACCCCAAT	GCTCGAGATAAT 30 590
649550	-		CCAGGCTGCT		CAGGGAGGAGCT	LO 520 rGGGTTTCCGGC
-	TGGAATTA	TACTCCTCT			AAGGAAAGATTO	GATGTTTGC 640
649550	CCGAGTAC	AGTGCGAGT	CAGCTCAAG			570 FACAGAGGATAA
_			TACAGCATGO		ACCATCCGAAA	FACAGATGG-AA 690
649550				AGG	610 AGTCAAGAGTGA ::: :::	AAGGAAAGAGAA
-	GGACAGCA 700	TTGGATTTA 710	GCAGATCCAT 720	CTGCCAAAGC 730	AGTGCTTACTG0 740	GTGAATATAAGA 750
649550	630 AAGGCGAT	GAGGTGGAT	GGAGTGGAT	660 GAAGTGGCGAA		670 TCTAAA ::::
-	AAGATGAA 760	770	780	790	GAAGAAAAAAT( 800	SATGGCTCTACT 810
 649550	760 68	770 0 AAAAAGACA	780 690	790 700 PAAGCTTGAAA	710	810 720 GCTCAGAACGAC
 649550 	760 68 AAAG : :	770  AAAAAGACA :::::::: TAAATGTCA	780 690 AGGATAGT : : : ACTGCCACGO	790 700 PAAGCTTGAAA ::: :::	800 710 AAGCCCTAAAGC : : :::: -TGGCAGAAAG	810 720 GCTCAGAACGAC
 7	760 68 AAAG : : CACACCAT 820 30 CTGATCTG	770 0 AAAAAGACA :::::::: TAAATGTCA 830	780 690 AGGATAGT : : : ACTGCCACGC 840 750 GGACGAGCTA	790 700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT	800 710 AAGCCCTAAAGC : : :::: -TGGCAGAAAG- 850 770 GTTCAACT	810 720 GCTCAGAACGAC ::: ::TCAACTCCAT
 7	760  68  AAAG : : CACACCAT 820  30 CTGATCTG :: ::	770  O AAAAAGACA :::::::: TAAATGTCA 830  740 GAACATCAA	780 690 AGGATAGT : : : ACTGCCACGG 840 750 AGGACGAGCTA	790 700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT	800 710 AAGCCCTAAAGC : : :::: -TGGCAGAAAG- 850 770 GTTCAACT	810 720 GCTCAGAACGAC :::::::TCAACTCCAT 860 780 AATGACCTGA
 7 649550 	760  68 AAAG : : : CACACCAT 820  30 CTGATCTG :: :: TACATTTG 870  790	770  0 AAAAAGACA :::::::: TAAATGTCA 830  740 GAACATCAA ::::::: GG-CAGCAG 880  800 CTCATCTTC	780 690 AGGATAGT : : : ACTGCCACGG 840 750 AGGACGAGCTA : : : GGATATAACAG 890	790 700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGT : ::: : GAGTAAAGATT 900	800 710 AAGCCCTAAAGC :::::: -TGGCAGAAAG- 850 770 GTTCAACTA :::::: GTACAGCTGTTA 910  820 820 CCTTCTGGGGAA	810 720 GCTCAGAACGAC ::: :::TCAACTCCAT 860 780 AATGACCTGA ::: ::: ACTGCAACATGG
 7 649550 	760  68 AAAG : : : CACACCAT 820  30 CTGATCTG :: :: TACATTTG 870  790 AGGAGCTA :: : :	770  0 AAAAAGACA :::::::: TAAATGTCA 830  740 GAACATCAA :::::::::::::::::::::::::::::::	780 690 AGGATAGT : : : ACTGCCACGG 840 750 AGGACGAGCTA : : : GGATATAACAG 890 810 CAACAAGCAG	790 700 TAAGCTTGAAA ::: ::: CAAGTGA 760 AAAGAAAGTGTG : ::: : GAGTAAAGATTG 900CAAGTGG : :::	800 710 AAGCCCTAAAGC :::::: -TGGCAGAAAG- 850 770 GTTCAACT	810 720 GCTCAGAACGAC :::::::TCAACTCCAT 860 780 AATGACCTGA ::::::: ACTGCAACATGG 920 830 GTCGGCGATCTT
- 649550 - 649550	760  68 AAAG : : : CACACCAT 820  30 CTGATCTG :: :: TACATTTG 870  790 AGGAGCTA :: : : AGCTGATC 930  840	770  0 AAAAAGACA :::::::: TAAATGTCA 830  740 GAACATCAA :::::::::::::::::::::::::::::::	780 690 AGGATAGT : : : ACTGCCACGG 840 750 AGGACGAGCTA : : : GGATATAACAG 890 810 CAACAAGCAG : : : : AAGATAAAGG 950  60 86	790 700 7AAGCTTGAAAI ::: ::: CAAGTGA 760 AAAGAAAGTGTG : ::: : GAGTAAAGATTG 900CAAGTG : ::: GTGATCTGGTAG 960	800 710 AAGCCCTAAAGC :::::: -TGGCAGAAAG- 850 770 GTTCAACT	810 720 GCTCAGAACGAC ::: ::TCAACTCCAT 860 780 AATGACCTGA ::: ::: ACTGCAACATGG 920 830 GTCGGCGATCTT : :::: ATGCCTGTTCTT
- 649550 - 649550	760  68 AAAG : : : CACACCAT 820  30 CTGATCTG :: :: TACATTTG 870  790 AGGAGCTA :: : : AGCTGATG 930  840GGACCG :: :	770  0 AAAAAGACA :::::::: TAAATGTCA 830  740 GAACATCAA :::::::::::::::::::::::::::::::	780 690 AGGATAGT : : : ACTGCCACGG 840 750 AGGACGAGCTA : : : GGATATAACAG 890 810 CAACAAGCAG- :: : :: AAGATAAAGG 950  00 86 AGCCGATGGCA	790 700 7AAGCTTGAAA ::::::: CAAGTGA 760 AAAGAAAGTGT ::::::: GAGTAAAGATT 900CAAGTG ::::: GTGATCTGGTA 960 ATGGTGTT	800 710 AAGCCCTAAAGC ::::::: -TGGCAGAAAG- 850 770 GTTCAACT	810 720 GCTCAGAACGAC :::::::TCAACTCCAT 860 780 AATGACCTGA ::::::: ACTGCAACATGG 920 830 GTCGGCGATCTT :::::: ATGCCTGTTCTT 980 880 GTCCCTGCGAGG

-		GTGGCAATT		rcatgag-g	:: : : CAGCTTCTA 1080	AGAACAGGG	
649550		TGGACCAAG'	TGTATGGTC	AAGACACAG	80 ACACCC	AACCGG	
_	TGTTCTC	TTCTCTTAA	GTTATGGTG	CAGACCCA-	ACACTGCTC 1140	AATTGTCAC	
649550		GAGTGGGTA	ACCCCAAAG	GAATTCCGA	103 GAAATCTCT ::::	TACCTCAAG	AAATTGAA
- 11	TGCTATA	GACTTGGCT	CCCACACCA	CAGTTAAAA	GAAAGAT 1200	TAGCATATG	AATTTAAA
649550		;		<b>-</b> CGT	1070 ATATTCCCC	CCAGAA	ACCAGCGC
_		CGTTGCTGC	AAGCTGCAC	GAGAAGCTG	:: :: : : ATGTTACTC 1260	GAATCAAAA	AACATCTC
	-CTCCG-	TGGCGG		CTCCGCCCT	CCA		CTCCTGCT
-	TCTCTGG	AAATGGTGA	ATTTCAAGC.	ATCCTCAAA	: : CACATGAAA 1320	CAGCATTGC	ATTGTGCT
649550	GCTGTGA	ACTCC-TCT	GCTTCAGCA	GATAAGCCA	170 TTATCCAAC	ATGAAGATC	CTGACTCT
	GCTGC-A		CCCAAAA	GA-AAGCAA	::: ATAT 370	GTGAA	
649550		CTGTCCCGG	AACAAGGAT	GAAGTGAAG	230 GCCATGA	TTGAGAAAC	TCGGGGGG
-		GG	AGCAAACAT	CAATGAAAA	: : : :: .GACTAAAGA 1420	ATTCTTGAĊ	TCCTCTGC
649550	AAGTTGA		GGCCAACAA	GGCTTCCCT	·		
-	ACGTGGC	: : :: ATCTGAGAA 1450	AGCTCATAA'	TGATGTTGT	TGAAGTAGT 1480	GGTGAAACA	
649550	AAA		AAAGATGAA	TAAGA		AGA	
_	AGGTTAA'		TAATCTTGG	TCAGACTTC	TCTACACAG 1540	AGCTGCATA	
649550	GTAAAGG		CCAACATCC	GAGTTGTGT	CTGAGGACT		
	: : ATCTACA 1560	AACCTGCCG		GAGCTATGG	:: : : GTGTGATCC 1600	TAACATTAT	
1 649550	AGGACGT		CACCAAGAG	CCTT		GTTGTTCTT	'AGCGCACA
-				AAATGAAAA	:::: TGTACAGCA		AGAGGGTA
				1000	1000	107	O

_	::: : : TCTCATTAGGTAA	: :::::: TTCAGAGGCAGA	: CAGACAATTG	:: ::: : CTGGAAGCTG	CAAAGGCTGGAGATG
_	1680 1690	1700	1710	1720	1730
649550 -	: : :: TCGAAACTGTAAA	AGGGAAG : ::	TCAGGGG : :::: TGTTCAGAG-	:: :: -TGTCAACTG	CAAAAAAAGC-AAGG :: : : :::: CAGAGACATTGAAGG
					1560 1570
649550					CTGAAAAGAGAATGA :: ::
-	GCGTCAGTCTACA		GCAGCTGGGT	'AT-AACAGAG	-TGTCCGTGGTGG
649550		1590 AGGA-GGAGCAG			1620 GGACTGGAACAC
_		AGCATGGAGCTG	ATGTGCATGC		::: :: :: :: :: :: :: :: :: :: :: :: ::
649550	1630 TCTGCGCA	1640 TGTCCTGGA			TCTT
049550	: ::: :::	::: :: :::	: :::	:: :::	::::
- 19	PITTGCACAATGCA				TCTTGTTAAACATGG 1960
649550			TGGACAT	CGTTAAA	GGAACCAACTCCTAC
- 1 ¢	AGCAGTAGTTAAT		TGGAAATTTA	CACCTTTACA	TGAAGCAGCAGCAAA
	70 1980	1000	2000	2010	2020
		1710 TACAAGCTG	1720 CAGCTTC	1730 TGGAGGA	1740 CGAC-AAGGAAAA
649550	)	1710 TACAAGCTG : ::: :: ATTTGCAAACTT	1720 CAGCTTC : ::: :	1730 TGGAGGA :::::	1740CGAC-AAGGAAAA : :: :: ::::
649550	AGGAAAATATGAA 330 2040 1750	1710 TACAAGCTG : ::: :: ATTTGCAAACTT 2050 1760	1720 CAGCTTC: :::::: CTGCTCCAGC 2060	1730 TGGAGGA ::: : : CATGGTGCAGA 2070 1780	1740 CGAC-AAGGAAAA : :: :: :::: CCCTACCAAAAAAA 2080
649550	AGGAAAATATGAA 330 2040 1750	1710 TACAAGCTG : ::: :: ATTTGCAAACTT 2050 1760 PATTCAGGT	1720 CAGCTTC : ::: : CTGCTCCAGC 2060 1770 CCTGGGGCCG	1730 -TGGAGGA :::::: CATGGTGCAGA 2070 1780 G-TGTGGGTAC	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080
649550	AGGAAAATATGAA 330 2040 1750 CAGGTATTGGA-T	1710TACAAGCTG : ::: :: ATTTGCAAACTT 2050 1760 PATTCAGGT	1720 CCTGCTCCAGC 2060  1770 CCTGGGGCCG : :: :	1730 -TGGAGGA :::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC :::::::	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080  GGTGATCG : ::::
649550 - 20 649550 - 20	AGGAAAATATGAA 330 2040 1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG : ::: :: ATTTGCAAACTT 2050  1760 'ATTCAGGT : :: :: 'ACTCCTTTGGAT 2110	1720 CAGCTTC : ::: : CTGCTCCAGC 2060 1770 CCCTGGGGCCG : :: : CCTTGTTAAAG 2120	1730 -TGGAGGA :::::: CATGGTGCAGA 2070 1780 G-TGTGGGTAC ::::::: CATGGAGATAC 2130	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080  GGTGATCG : ::::
649550 - 20 649550 - 20	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG : ::: :: ATTTGCAAACTT 2050  1760 CATTCAGGT : :: :: CACTCCTTTGGAT 2110  1800 1800 1800 1800 1800 1800 180	1720 ::::::::::::::::::::::::::::::::::::	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGATAC CAAGGAGATAC	1740CGAC-AAGGAAAA : :: :: :::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: ::
649550 - 20 649550 - 20 17 649550	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG : ::: :: ATTTGCAAACTT 2050  1760 CATTCAGGT : :: :: CACTCCTTTGGAT 2110  1800 1800 1800 1800 1800 1800 180	1720 CCAGCTTC : ::: : CCTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CCTTGTTAAAG 2120  10 18 GGATGCCGTCC :::: :: ::	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGATAC CAAGGAGATAC	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080  CGGTGATCG : :::: CAGATATTCAAGATCT 2140  1830GCCATTGAGC
649550 - 20 649550 - 20 649550 - 21	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::: CAGGGATGGAAAT 90 2100  90 G-TAGCAA :::::::::: GCTTAGGGGAGAT 50 2160  1840	1710TACAAGCTG ::::::: ATTTGCAAACTT 2050  1760 PATTCAGGT :::::::: PACTCCTTTGGAT 2110  1800 1800 1800 1800 1800 1800 180	1720 CCAGCTTC : ::: : CCTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CCTTGTTAAAG 2120  10 18 GATGCCGTCC :::: :: :: GATGCTG-CC 2180  1850	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGGAT- :::::::: CAAGAAGGGTT 2190	1740CGAC-AAGGAAAA : :: :: :::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: : GTTTAGCCAGAGTGA 2200  1860
649550 - 20 649550 - 21 649550	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::: CAGGGATGGAAAT 90 2100  90 G-TAGCAA :::::::::: GCTTAGGGGAGAT 50 2160  1840	1710TACAAGCTG ::::::: ATTTGCAAACTT 2050  1760 PATTCAGGT :::::::: PACTCCTTTGGAT 2110  1800 1800 1800 1800 1800 1800 1700 1800 18	1720 CCAGCTTC : ::: : CTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CTTGTTAAAG 2120  10 18 GATGCCGTCC :::: : :: GATGCTG-CC 2180  1850 AAATT	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGGAT- :::::::: CAAGAAGGGTT 2190	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: : GTTTAGCCAGAGTGA 2200  1860 GAAGAAAAAACC
649550 - 20 649550 - 21 649550	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG : ::: :: ATTTGCAAACTT 2050  1760 PATTCAGGT : :: :: PACTCCTTTGGAT 2110  1800 18 ACAAACTGGAACA : :: :: PGCAGCTTTGCTA 2170  CATG- ::: CTCCTGATAATGT	1720 CCAGCTTC : ::: : CTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CCTTGTTAAAG 2120  10 18 GATGCCGTCC 2180  1850 AAATT :::::	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGATAC 2130  CAAGGAGGAT- ::::::: CAAGAAGGGTT 2190 ATAT :::	1740CGAC-AAGGAAAA : :: :: ::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: : GTTTAGCCAGAGTGA 2200  1860 GAAGAAAAAACC
649550 - 20 649550 - 21 649550 - 21	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG ::::::: ATTTGCAAACTT 2050  1760 PATTCAGGT :::::::: PACTCCTTTGGAT 2110  1800 1800 180 CAAACTGGAACA ::::::::: PGCAGCTTTGCTA 2170  CATG- ::: CTCCTGATAATGT 2230  CACTCCAA	1720 CCAGCTTC : ::: : CTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CTTGTTAAAG 2120  10	1730 -TGGAGGA :::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGATAC 2130  CAAGGAGGAT- ::::::: CAAGAAGGGTT 2190 ATAT ::: CGATACCCAAG 2250  1900  CAAGTATCCCA	1740CGAC-AAGGAAAA : :: :: :::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: :: GTTTAGCCAGAGTGA 2200  1860 GAAGAAAAAACC : :: : :: GCAGACATTCAACAC 2260  1910 1920 AAAAGTTCTACCCCC
649550 - 20 649550 - 21 649550 - 21	AGGAAAATATGAA 30 2040  1750 CAGGTATTGGA-T ::::::::::::::::::::::::::::::::::::	1710TACAAGCTG ::::::: ATTTGCAAACTT 2050  1760 PATTCAGGT :::::::: PACTCCTTTGGAT 2110  1800 1800 1800 1800 CAAAACTGGAACA :::::::::::::::::::::::::::::::::	1720 CCAGCTTC : ::: : CCTGCTCCAGC 2060  1770 CCCTGGGGCCG : :: : CCTTGTTAAAG 2120  10	1730 -TGGAGGA ::::::: CATGGTGCAGA 2070  1780 -TGTGGGTAC ::::::: CATGGAGATAC 2130  CAAGGAGATAC 2130  CAAGGAGGAT- ::::::: CAAGAAGGGTT 2190  -ATAT ::: CGATACCCAAG 2250  1900 CAAGTATCCCA	1740CGAC-AAGGAAAA : :: :: :::: CCCTACCAAAAAAAA 2080  GGTGATCG : :::: AGATATTCAAGATCT 2140  1830GCCATTGAGC :::: :: GTTTAGCCAGAGTGA 2200  1860 GAAGAAAAAACC : :: : :::::::::::::::::::::::::::

649550	1930 TGGAGATTGACTA			1950 AGGCAG
-				: i::: TTACATAATGCAGCATC 2380
649550		rgaagaagctg		1980 CCTGGCACCAA : :: :: ::
-		rgtagcagctctact.	AATAAAGTATAATO	CATGTGTCAAŢGCCAC
649550	GTCCAAGCTCC		AC-CTCATCAAGAT	2030 CGATCTTT : ::::
_	GGACAAATGGGCTTT		AAGCAGCCCAAAA	GGACGAACACAGCTTT
649550	: ::::::::	::: ::	:::	CCATGGTGGAGTA
_		CCCATGGAGCTGACC 2530		CAGGAAGGACAAACAC 50 2560
649550	TGAGATCGACCTT	CAGAAGATG		00 2110 AGCTGAGCAAAAGGCAG
-	CTTTAGATTTAGTTTC 2570 2580	CAGCGGATGATGTCA 2590 -	GCGCTCTTCTGACA 2600 261	AGCAGCCATGCCCCC LO 2620
64,9550			TCCTCAGTGAG	STCCAGCAGGCGGTGTC
-		TTGTTACAAGCCTCA 40 2650		GTG-AGAAGCCCAGGAG 2670 2680
649550 —	TCAGGGCAGCAGCGA :: :::: :: CCACTGCAGATGCTC	:::: ::: ::: :	GGATCTCTCAAAT( : : : : : : : : : : : : : : : : : : :	CGCTTTTACACCCTG-A : :: : : : : : CCTTTCTGCAGCCAGCA
	220 2230 TCCCCCACGACTT			CCTGAA
	GTCTTGACAACTTAT	::::: : :: CTGGGAGTTTTTCAG 760 2770		: ::: AGTTAGTTCAAGTGGAA 2790 2800
22 649550	CAATGCAGACA	0 2280 GTGTGCAGGCCAAGG :: :: :: :::		
_		GTTTGGAGAAAAAGG 820 2830	AGGTTCCAGGAGTA 2840	AGATTTTAGCATAACTC 2850 2860
	290 AATGC			2320 2330 GGTG-GCCTACAGTCTG :::::::::
_	AATTCGTAAGGAATC			rgagagagaacagatca 2910 2920
649550		GATGATAGCAG		GATGTCAAC
-	CTTTGGAT-GTATTA			GAGATTGGAATCAATGC 2970 2980

	-TATGAGAAG		ATTAAGGTGGT	rgacagagat-t	CTGAAGAAGCCG
-	TTATGGACATAGGG		-TTAAAGGAGT(		CTCCGGACAACA
649550	AGATCATCAGGAAG		-GAACAC	TCATGCAACC	
	AGGTCTTAACCCA 3040 3050	-TAT-TTAACTT	TGAACACCTCT	GTAGTGGAACA.	
649550		2480 24 ACAATGCGTATG	ACTTGGA		2500 AGT-CATCGA
-	CTGTCTCCTGATGA	ATAAAGAGTTTC	AGTCTGTGGAG	GAAGAGATGCAA.	AGTACAGTTCGA
649550	TATCTTTAAGATA		GCGAATGC	CAGCGTTACAAG	
_	GAGCACAGAGATG		GTGGAATCTTC	AACAGATACAAT.	ATTCTCAAGATT
649550	2560 2 AAGCAGCTTCATAA		TGTGGCACGGG	rccagg.	
_	CAGAAGGTTTGTAZ 3220 323	ACAAGAAA-C	TATGGGAAAGA'		
649550	CC2	00 2 ACCAACTTTGC-	TGGGAT	CCTGTCCCA-GG	GTCTTCG
-	TCTGAAGAAAACCA 3280	AC-AACCATGCC 3290	AATGAACGAAT0 3300 3:	GCTATTTCATGG 310 332	GTCTCCTTTTGT 0 3330
649550	2640 GATAGCO :: :::	JCCGCCT	GAAGCGCC		CTACATGTTTGG
-	GAATGCAATTATC		GATGAAAGGCA'	rgcgtacatagg	TGGTATGTTTGG
649550	2680 269 TAAAGGGATCTAT		GTCTCCAAGAG'	TGCCAACTACTG	CCATACGTCTCA
-	AGCTGGCATTTAT	PTTGCTGAAAAC	TCTTCCAAAAG	CAATCAATAT	
649550	2740 275 GGGAGACCCAATAG	GGCTTAATCCTG	TTGGG		
- 345	GGAGGAGGTACTG 50 3460		TTCACAAAGACA 3480		
649550	2790 280 TATGAACTGAAC	GCACGCTTCACA	TATCAGCAAGT	TACCCA	
_ ·	CAGCTGCTCTTTTC		T-TGGGAAAGT	CTTTCCTGCAGT	· ·
	2840 2850 CAGTGTCAAAGGT		860 : AAACTACCC		CAG
_	: :: :: : AAATGGCACATTC	: ::::	::: :	::: : ::	:::

3570	3580	3590	3600	3610	3620
2880 649550 -CTAACA		2900 GTGTAGACGI		2920 ACCGGGATT	2930 CATCTGGTGTG
CCTAGCA	:::: ::: :: FTAG-CTGAATA	:: TGTTATT	::::::::::::::::::::::::::::::::::::::	: : :: :: BAACAGGCTT-	::: ::: ATCCTGAGTA
3630				660	3670
2940 649550 AATGACAG		2960 ATAACGAGTA	297 ACAT • • • • • • • • • • • • • • • • • • •	-	2980 ATATTGCTCA
- TTTAATT7	 ACTTACCAG 3690	ATTATGAGGO 3700	CCTGAAGGTAT 3710	GGTCGATGGA 3720	ATAAATAGTTAT 3730
2990 649550 GGTAAAT0	3000	3010	3020	. <b>7</b>	
:::	:: :: ::	:::::::	: :::: :::	:	:
_ TTTAAGA- 3740	AACTAATTC 375				
3030 649550 TTTAAGA	3040 CCTCCCTGTGGT	· • • • • • • • • • • • • • • • • • • •			
::::	: : ::: CTTTGCTGAAAA	::			
31	300 381	.0		•	